



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/783,672
Source: IFW
Date Processed by STIC: 8/19/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
~~VERSION 4.2 PROGRAM ACCESSIBLE THROUGH THE U.S. PATENT AND~~
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10783672

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) 1,2 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/783,672

TIME: 15:14:43

Input Set : D:\53279-20003.00 - Seqlist.txt

Output Set: N:\CRF4\08192004\J783672.raw

**Does Not Comply
Corrected Diskette Needed**

Xaa can only represent a
single amino acid
(see item 5 on
Error summary sheet)

see item 5

RAW SEQUENCE LISTING

DATE: 08/19/2004

PATENT APPLICATION: US/10/783,672

TIME: 15:14:43

Input Set : D:\53279-20003.00 - Seqlist.txt

Output Set: N:\CRF4\08192004\J783672.raw

```

--> 65 <400> 2
--> 66 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
67 1 5 10 15
68 Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
69 20 25 30
70 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
71 35 40
74 <210> SEQ ID NO: 3
75 <211> LENGTH: 33
76 <212> TYPE: PRT
77 <213> ORGANISM: Homo sapiens
79 <220> FEATURE:
80 <221> NAME/KEY: DNA BIND
81 <222> LOCATION: 3-6, 13-14, 21, 29, 31
82 <223> OTHER INFORMATION: Xaa = any amino acid
84 <400> SEQUENCE: 3
--> 85 Lys Arg Xaa Xaa Xaa Xaa Arg Lys Ser Ala Gln Asn Xaa Xaa Ser Ala
86 1 5 10 15
87 Gln Ser Ala Gln Xaa Arg Lys Thr Ala Glu Asn Gln Xaa Arg Xaa Arg
88 20 25 30
89 Lys

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/783,672

DATE: 08/19/2004
TIME: 15:14:44

Input Set : D:\53279-20003.00 - Seqlist.txt
Output Set: N:\CRF4\08192004\J783672.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. ~~1,2,4,6,7,8,9,10,11,12,13,14,16,17,19~~
Seq#:2; Xaa Pos. ~~2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,19,20,22,24,25,26,27~~
Seq#:2; Xaa Pos. ~~28,30,31,32,33,34,35,36,37,38,40,41~~
Seq#:3; Xaa Pos. ~~3,4,5,6,13,14,21,29,31~~

VERIFICATION SUMMARY

DATE: 08/19/2004

PATENT APPLICATION: US/10/783,672

TIME: 15:14:44

Input Set : D:\53279-20003.00 - Seqlist.txt

Output Set: N:\CRF4\08192004\J783672.raw

L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:40 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:65 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3